

## Raw Sequence Listing Error Summary

ERROR DETECTEDSUGGESTEDCORRECTIONSERIAL NUMBER: 09/383,894A  
4-10-01**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".

2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".

3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.

4 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 Variable Length Sequence(s) \_\_\_\_\_ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

8 Skipped Sequences (OLD RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
**(2) INFORMATION FOR SEQ ID NO:X:**  
**(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")**  
**(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:**  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 Skipped Sequences (NEW RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000

10 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 Use of <213>Organism (NEW RULES) Sequence(s) \_\_\_\_\_ are missing this mandatory field or its response.

12 Use of <220>Feature (NEW RULES) Sequence(s) \_\_\_\_\_ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

R. Lacourrieu

1635

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/383,894A

DATE: 03/30/2001  
 TIME: 15:37:27

Input Set : A:\00400191.app  
 Output Set: N:\CRF3\03302001\I383894A.raw

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 5 <120> TITLE OF INVENTION: T-Type Calcium Channel  
 7 <130> FILE REFERENCE: 004.00191  
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 10 <141> CURRENT FILING DATE: 1999-08-26  
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 13 <151> PRIOR FILING DATE: 1998-08-26  
 15 <150> PRIOR APPLICATION NUMBER: US 60/117,399  
 16 <151> PRIOR FILING DATE: 1999-01-27  
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P. b  
 Does Not Comply  
 Corrected Diskette Needed

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION: US/09/383,894A**

**DATE: 03/30/2001**  
**TIME: 15:37:27**

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**Output Set: N:\CRF3\03302001\I383894A.raw**

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**RAW SEQUENCE LISTING**  
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**DATE: 03/30/2001**  
**TIME: 15:37:27**

**Input Set : A:\00400191.app**  
**Output Set: N:\CRF3\03302001\I383894A.raw**

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168	65							70			75					80
170	Pro	Trp	Phe	Glu	Arg	Val	Ser	Met	Leu	Val	Ile	Leu	Leu	Asn	Cys	Val
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173	Thr	Leu	Gly	Met	Phe	Arg	Pro	Cys	Glu	Asp	Ile	Ala	Cys	Asp	Ser	Gln
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177								115			120					125
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189								180			185					190
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 255 530 535 540  
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 278 Ala Asp Ser Gly Ala Cys Gly Pro Asp Ser Cys Pro Tyr Cys Ala Arg  
 279 660 665 670  
 281 Thr Gly Ala Gly Glu Pro Glu Ser Ala Asp His Val Met Pro Asp Ser  
 282 675 680 685  
 284 Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln His Ser Asp  
 285 690 695 700  
 287 Leu Arg Asp Pro His Ser Arg Arg Arg Gln Arg Ser Leu Gly Pro Asp  
 288 705 710 715 720  
 290 Ala Glu Pro Ser Ser Val Leu Ala Phe Trp Arg Leu Ile Cys Asp Thr  
 291 725 730 735  
 293 Phe Arg Lys Ile Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile Met Ile  
 294 740 745 750  
 296 Ala Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His Glu Gln  
 297 755 760 765  
 299 Pro Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr  
 300 770 775 780  
 302 Ser Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr Gly Pro  
 303 785 790 795 800  
 305 Phe Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val Ile Val  
 306 805 810 815  
 308 Val Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Leu Ser

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6

<210> 6  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer  
Sequence

<400> 6  
~~tmgchatgg a gmgnccy~~

→ see Item 10 on  
Error Summary  
sheet

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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/383,894A

DATE: 03/30/2001

TIME: 15:37:28

Input Set : A:\00400191.app

Output Set: N:\CRF3\03302001\I383894A.raw

L:1216 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6

L:1216 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6

L:1216 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6